Re-run

<u>RAW SEQUENCE LISTING</u>

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: <u>10/536,935 A</u>
Source: <u>   /FW</u>
Date Processed by STIC: <u>   6/8/06</u>

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RAW SEQUENCE LISTING   DATE: 08/08/2006
PATENT APPLICATION: US/10/536,935A   TIME: 18:09:06

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          Output Set: N:\CRF4\08082006\J536935A.raw

 1 <110> APPLICANT: Tsukahara, Kappei
 2   Tsuchiya, Mamiko
 3   Jigami, Yoshifumi
 4   Nakayama, Kenichi
 5   Umemura, Mariko
 6   Okamoto, Michiyo
 7 <120> TITLE OF INVENTION: METHOD OF SCREENING FOR COMPOUNDS THAT
 8   INHIBIT THE ENZYMATIC ACTIVITY OF GWT1 GENE PRODUCT
 9 <130> FILE REFERENCE: 082368-004400US
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/536,935A
11 <141> CURRENT FILING DATE: 2005-05-20
12 <150> PRIOR APPLICATION NUMBER: PCT/JP03/14909
13 <151> PRIOR FILING DATE: 2003-11-21
14 <150> PRIOR APPLICATION NUMBER: JP 2002-339418
15 <151> PRIOR FILING DATE: 2002-11-22
16 <160> NUMBER OF SEQ ID NOS: 18
17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1497
21 <212> TYPE: DNA
22 <213> ORGANISM: Saccharomyces cerevisiae
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (1)..(1494)
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28   Met Ala Thr Val His Gln Lys Asn Met Ser Thr Leu Lys Gln Arg Lys
29   1   5   10   15
30   gag gac ttt gtg aca ggg ctc aat ggc ggt tct ata aca gaa att aac   96
31   Glu Asp Phe Val Thr Gly Leu Asn Gly Gly Ser Ile Thr Glu Ile Asn
32   20   25   30
33   gca gtg aca tca att gct ttg gta act tac ata tca tgg aac tta ttg   144
34   Ala Val Thr Ser Ile Ala Leu Val Thr Tyr Ile Ser Trp Asn Leu Leu
35   35   40   45
36   aaa aat tcc aac ctt atg cct cct ggc att tcc agc gtg caa tac ata   192
37   Lys Asn Ser Asn Leu Met Pro Pro Gly Ile Ser Ser Val Gln Tyr Ile
38   50   55   60
39   att gat ttt gca ttg aac tgg gtt gct ttg ctt cta tct att act att   240
40   Ile Asp Phe Ala Leu Asn Trp Val Ala Leu Leu Leu Ser Ile Thr Ile
41   65   70   75   80
42   tat gct agt gaa cca tac ctt cta aac acg cta ata ctg tta cct tgt   288
43   Tyr Ala Ser Glu Pro Tyr Leu Leu Asn Thr Leu Ile Leu Leu Pro Cys
44   85   90   95

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45    ttg ctc gca ttc ata tat gga aaa ttt act agc tcg agt aaa cct tct   336
46    Leu Leu Ala Phe Ile Tyr Gly Lys Phe Thr Ser Ser Ser Lys Pro Ser
47                100                 105                 110
48    aat cca ata tac aat aaa aaa aaa atg att aca cag cgg ttc caa cta   384
49    Asn Pro Ile Tyr Asn Lys Lys Lys Met Ile Thr Gln Arg Phe Gln Leu
50                115                 120                 125
51    gaa aaa aag ccg tat att act gcg tat cgt ggt ggg atg ctt att ctg   432
52    Glu Lys Lys Pro Tyr Ile Thr Ala Tyr Arg Gly Gly Met Leu Ile Leu
53                130                 135                 140
54    act gct att gcc atc ttg gct gta gat ttt cca att ttc cca agg agg   480
55    Thr Ala Ile Ala Ile Leu Ala Val Asp Phe Pro Ile Phe Pro Arg Arg
56    145                 150                 155                 160
57    ttt gcc aag gtg gaa act tgg ggg aca tcc ctg atg gat ctt ggt gta   528
58    Phe Ala Lys Val Glu Thr Trp Gly Thr Ser Leu Met Asp Leu Gly Val
59                165                 170                 175
60    gga tca ttc gtt ttc agt aac ggt att gtt tct tct agg gca ctg ttg   576
61    Gly Ser Phe Val Phe Ser Asn Gly Ile Val Ser Ser Arg Ala Leu Leu
62                180                 185                 190
63    aaa aac cta agc ttg aag agt aaa ccc agc ttc tta aaa aat gca ttt   624
64    Lys Asn Leu Ser Leu Lys Ser Lys Pro Ser Phe Leu Lys Asn Ala Phe
65                195                 200                 205
66    aat gcc tta aaa tca gga gga act cta ttg ttc cta gga ttg ctg agg   672
67    Asn Ala Leu Lys Ser Gly Gly Thr Leu Leu Phe Leu Gly Leu Leu Arg
68                210                 215                 220
69    ttg ttt ttt gta aaa aat ttg gaa tat caa gaa cat gtc aca gaa tat   720
70    Leu Phe Phe Val Lys Asn Leu Glu Tyr Gln Glu His Val Thr Glu Tyr
71    225                 230                 235                 240
72    ggg gtt cat tgg aat ttt ttt atc acc cta tca ttg ttg cca ctt gta   768
73    Gly Val His Trp Asn Phe Phe Ile Thr Leu Ser Leu Leu Pro Leu Val
74                245                 250                 255
75    ttg acc ttt att gat ccc gtc aca aga atg gtt cca cgc tgc tca att   816
76    Leu Thr Phe Ile Asp Pro Val Thr Arg Met Val Pro Arg Cys Ser Ile
77                260                 265                 270
78    gca ata ttc att tca tgc att tat gaa tgg cta ctt tta aag gac gat   864
79    Ala Ile Phe Ile Ser Cys Ile Tyr Glu Trp Leu Leu Leu Lys Asp Asp
80                275                 280                 285
81    cgc act tta aac ttt tta att ttg gct gat aga aat tgt ttc ttc agt   912
82    Arg Thr Leu Asn Phe Leu Ile Leu Ala Asp Arg Asn Cys Phe Phe Ser
83                290                 295                 300
84    gct aat aga gaa ggc atc ttc tca ttt cta ggt tat tgc tcg att ttt   960
85    Ala Asn Arg Glu Gly Ile Phe Ser Phe Leu Gly Tyr Cys Ser Ile Phe
86    305                 310                 315                 320
87    ctt tgg ggc caa aac acg gga ttt tac ttg ttg gga aat aaa cca act   1008
88    Leu Trp Gly Gln Asn Thr Gly Phe Tyr Leu Leu Gly Asn Lys Pro Thr
89                325                 330                 335
90    tta aac aat ctt tat aag cct tct acg caa gac gta gtt gca gca tca   1056
91    Leu Asn Asn Leu Tyr Lys Pro Ser Thr Gln Asp Val Val Ala Ala Ser
92                340                 345                 350
93    aag aag tct tcg act tgg gac tat tgg act tca gta acc cca tta agt   1104
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94        Lys Lys Ser Ser Thr Trp Asp Tyr Trp Thr Ser Val Thr Pro Leu Ser
95                355                 360                 365
96        ggc ctc tgt ata tgg agt aca att ttt ctt gtt atc agc cag ttg gtt      1152
97        Gly Leu Cys Ile Trp Ser Thr Ile Phe Leu Val Ile Ser Gln Leu Val
98                370                 375                 380
99        ttt caa tac cat cct tat agt gtt tca aga agg ttt gct aac tta cca      1200
100        Phe Gln Tyr His Pro Tyr Ser Val Ser Arg Arg Phe Ala Asn Leu Pro
101        385                 390                 395                 400
102        tat act ttg tgg gtc att act tat aat tta cta ttt ttg act ggg tac      1248
103        Tyr Thr Leu Trp Val Ile Thr Tyr Asn Leu Leu Phe Leu Thr Gly Tyr
104                    405                 410                 415
105        tgc ttg act gac aaa att ttc ggt aat tct tcg gaa tat tat aaa gtt      1296
106        Cys Leu Thr Asp Lys Ile Phe Gly Asn Ser Ser Glu Tyr Tyr Lys Val
107                    420                 425                 430
108        gcc gaa tgc ttg gaa tca atc aac tcc aat ggg ttg ttt tta ttt ttg      1344
109        Ala Glu Cys Leu Glu Ser Ile Asn Ser Asn Gly Leu Phe Leu Phe Leu
110                435                 440                 445
111        ttg gca aat gtc tct act ggt tta gtc aat atg tct atg gtc acg ata      1392
112        Leu Ala Asn Val Ser Thr Gly Leu Val Asn Met Ser Met Val Thr Ile
113            450                 455                 460
114        gat tct tca ccc tta aaa tca ttc ctg gtt ttg ttg gca tac tgc tca      1440
115        Asp Ser Ser Pro Leu Lys Ser Phe Leu Val Leu Leu Ala Tyr Cys Ser
116        465                 470                 475                 480
117        ttc ata gct gtc ata tcg gtt ttc ttg tat aga aaa aga ata ttc att      1488
118        Phe Ile Ala Val Ile Ser Val Phe Leu Tyr Arg Lys Arg Ile Phe Ile
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120        aag cta taa                                                          1497
121        Lys Leu
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124 <211> LENGTH: 498
125 <212> TYPE: PRT
126 <213> ORGANISM: Saccharomyces cerevisiae
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130        Glu Asp Phe Val Thr Gly Leu Asn Gly Gly Ser Ile Thr Glu Ile Asn
131                    20                  25                  30
132        Ala Val Thr Ser Ile Ala Leu Val Thr Tyr Ile Ser Trp Asn Leu Leu
133                35                  40                  45
134        Lys Asn Ser Asn Leu Met Pro Pro Gly Ile Ser Ser Val Gln Tyr Ile
135            50                  55                  60
136        Ile Asp Phe Ala Leu Asn Trp Val Ala Leu Leu Leu Ser Ile Thr Ile
137        65                  70                  75                  80
138        Tyr Ala Ser Glu Pro Tyr Leu Leu Asn Thr Leu Ile Leu Leu Pro Cys
139                        85                  90                  95
140        Leu Leu Ala Phe Ile Tyr Gly Lys Phe Thr Ser Ser Ser Lys Pro Ser
141                    100                 105                 110
142        Asn Pro Ile Tyr Asn Lys Lys Lys Met Ile Thr Gln Arg Phe Gln Leu
143                115                 120                 125
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144      Glu Lys Lys Pro Tyr Ile Thr Ala Tyr Arg Gly Gly Met Leu Ile Leu
145          130             135             140
146      Thr Ala Ile Ala Ile Leu Ala Val Asp Phe Pro Ile Phe Pro Arg Arg
147      145             150             155             160
148      Phe Ala Lys Val Glu Thr Trp Gly Thr Ser Leu Met Asp Leu Gly Val
149          165             170             175
150      Gly Ser Phe Val Phe Ser Asn Gly Ile Val Ser Ser Arg Ala Leu Leu
151          180             185             190
152      Lys Asn Leu Ser Leu Lys Ser Lys Pro Ser Phe Leu Lys Asn Ala Phe
153          195             200             205
154      Asn Ala Leu Lys Ser Gly Gly Thr Leu Leu Phe Leu Gly Leu Leu Arg
155          210             215             220
156      Leu Phe Phe Val Lys Asn Leu Glu Tyr Gln Glu His Val Thr Glu Tyr
157      225             230             235             240
158      Gly Val His Trp Asn Phe Phe Ile Thr Leu Ser Leu Leu Pro Leu Val
159          245             250             255
160      Leu Thr Phe Ile Asp Pro Val Thr Arg Met Val Pro Arg Cys Ser Ile
161          260             265             270
162      Ala Ile Phe Ile Ser Cys Ile Tyr Glu Trp Leu Leu Leu Lys Asp Asp
163          275             280             285
164      Arg Thr Leu Asn Phe Leu Ile Leu Ala Asp Arg Asn Cys Phe Phe Ser
165          290             295             300
166      Ala Asn Arg Glu Gly Ile Phe Ser Phe Leu Gly Tyr Cys Ser Ile Phe
167      305             310             315             320
168      Leu Trp Gly Gln Asn Thr Gly Phe Tyr Leu Leu Gly Asn Lys Pro Thr
169          325             330             335
170      Leu Asn Asn Leu Tyr Lys Pro Ser Thr Gln Asp Val Val Ala Ala Ser
171          340             345             350
172      Lys Lys Ser Ser Thr Trp Asp Tyr Trp Thr Ser Val Thr Pro Leu Ser
173          355             360             365
174      Gly Leu Cys Ile Trp Ser Thr Ile Phe Leu Val Ile Ser Gln Leu Val
175          370             375             380
176      Phe Gln Tyr His Pro Tyr Ser Val Ser Arg Arg Phe Ala Asn Leu Pro
177      385             390             395             400
178      Tyr Thr Leu Trp Val Ile Thr Tyr Asn Leu Leu Phe Leu Thr Gly Tyr
179          405             410             415
180      Cys Leu Thr Asp Lys Ile Phe Gly Asn Ser Ser Glu Tyr Tyr Lys Val
181          420             425             430
182      Ala Glu Cys Leu Glu Ser Ile Asn Ser Asn Gly Leu Phe Leu Phe Leu
183          435             440             445
184      Leu Ala Asn Val Ser Thr Gly Leu Val Asn Met Ser Met Val Thr Ile
185          450             455             460
186      Asp Ser Ser Pro Leu Lys Ser Phe Leu Val Leu Leu Ala Tyr Cys Ser
187      465             470             475             480
188      Phe Ile Ala Val Ile Ser Val Phe Leu Tyr Arg Lys Arg Ile Phe Ile
189          485             490             495
190      Lys Leu
192 <210> SEQ ID NO: 3
193 <211> LENGTH: 1458
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RAW SEQUENCE LISTING   DATE: 08/08/2006
PATENT APPLICATION: **US/10/536,935A**   TIME: 18:09:06

Input Set : **N:\Crf4\Refhold\10_folder\J536935A.raw**
Output Set: **N:\CRF4\08082006\J536935A.raw**

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196  <220> FEATURE:
197  <221> NAME/KEY: CDS
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199  <400> SEQUENCE: 3
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202        1               5                  10                  15
203       act ggt ggc aca att gaa gaa att tat gct gta acc agt ata gca tta    96
204       Thr Gly Gly Thr Ile Glu Glu Ile Tyr Ala Val Thr Ser Ile Ala Leu
205                      20                  25                  30
206       tca tct tat ttg tcc ttt aga ttg ttg aaa aag tct ctt ggt gat tta   144
207       Ser Ser Tyr Leu Ser Phe Arg Leu Leu Lys Lys Ser Leu Gly Asp Leu
208                  35                  40                  45
209       gct ttg att tac gac tac att ctt aat gtg ttg aca att cta gca tcc   192
210       Ala Leu Ile Tyr Asp Tyr Ile Leu Asn Val Leu Thr Ile Leu Ala Ser
211           50                  55                  60
212       att act gtt tat agc aac agc cct tct tat ttg cat tat ttt att gtt   240
213       Ile Thr Val Tyr Ser Asn Ser Pro Ser Tyr Leu His Tyr Phe Ile Val
214        65                  70                  75                  80
215       att cca tca tta gtt ata tat cta gtg aat tac cat gtt gag aaa cca   288
216       Ile Pro Ser Leu Val Ile Tyr Leu Val Asn Tyr His Val Glu Lys Pro
217                      85                  90                  95
218       tct tca ccc cat aga caa aat gat aca aaa gaa gat aaa tcg gac gaa   336
219       Ser Ser Pro His Arg Gln Asn Asp Thr Lys Glu Asp Lys Ser Asp Glu
220                 100                 105                 110
221       cta ttg ccg aga aaa caa ttt ata aca gcc tat cgt tct caa atg ttg   384
222       Leu Leu Pro Arg Lys Gln Phe Ile Thr Ala Tyr Arg Ser Gln Met Leu
223                 115                 120                 125
224       ata att act aat cta gct ata tta gct gtt gat ttt cct att ttc cca   432
225       Ile Ile Thr Asn Leu Ala Ile Leu Ala Val Asp Phe Pro Ile Phe Pro
226           130                 135                 140
227       aga aga ttt gcc aaa gtg gaa aca tgg ggc acg tca atg atg gat tta   480
228       Arg Arg Phe Ala Lys Val Glu Thr Trp Gly Thr Ser Met Met Asp Leu
229       145                 150                 155                 160
230       gga gtt ggg tcg ttt gtg ttc tcc atg ggg ttg gct aat tct cga caa   528
231       Gly Val Gly Ser Phe Val Phe Ser Met Gly Leu Ala Asn Ser Arg Gln
232                 165                 170                 175
233       ttg atc aag aac cac acc gac aac tac aaa ttt agt tgg aag agt tat   576
234       Leu Ile Lys Asn His Thr Asp Asn Tyr Lys Phe Ser Trp Lys Ser Tyr
235                 180                 185                 190
236       ttg aaa aca atc aag cag aac ttt atc aag tca gtg cct ata ctt gtt   624
237       Leu Lys Thr Ile Lys Gln Asn Phe Ile Lys Ser Val Pro Ile Leu Val
238                 195                 200                 205
239       tta gga gct att cgt ttt gtt agt gtt aag caa ttg gac tat cag gaa   672
240       Leu Gly Ala Ile Arg Phe Val Ser Val Lys Gln Leu Asp Tyr Gln Glu
241           210                 215                 220
242       cac gaa aca gag tat gga atc cat tgg aat ttt ttc ttc aca tta ggg   720
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VERIFICATION SUMMARY   DATE: 08/08/2006
PATENT APPLICATION: **US/10/536,935A**   TIME: 18:09:07

Input Set : **N:\Crf4\Refhold\10_folder\J536935A.raw**
Output Set: **N:\CRF4\08082006\J536935A.raw**

L:10 M:270 C: Current Application Number differs, Wrong Format
L:1009 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 12, CDS
LOCATION:44..2001
L:1012 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 12, CDS
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L:1057 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 12, CDS
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L:1060 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 12, CDS
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L:1105 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 12, CDS
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